

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 01:30:23 ; Search time 366.45 Seconds
(without alignments)
3475.528 Million cell updates/sec

Title: US-09-205-015-3
Perfect score: 356
Sequence: 1.tcgaccctctggaacctatc.....atctggagctgaagaattc 356

Scoring table: IDENTITY_NUC

Searched: 808301 seqs, 1788773984 residues

Database : GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl1.*
- 9: gb_pl2.*
- 10: gb_pr1.*
- 11: gb_pr2.*
- 12: gb_pr3.*
- 13: gb_ro.*
- 14: gb_st.*
- 15: gb_sy.*
- 16: gb_un.*
- 17: gb_v1.*
- 18: gb_v2.*
- 19: em_ba.*
- 20: em_fun.*
- 21: em_hum1.*
- 22: em_hum2.*
- 23: em_in.*
- 24: em_ov.*
- 25: em_or.*
- 26: em_ov.*
- 27: em_pat.*
- 28: em_ph.*
- 29: em_pl.*
- 30: em_ro.*
- 31: em_sy.*
- 32: em_un.*
- 33: em_v1.*
- 34: em_v2.*
- 35: em_sts.*
- 36: gb_ba1.*
- 37: gb_ba2.*
- 38: gb_pl1.*
- 39: gb_pl2.*
- 40: gb_pr1.*
- 41: gb_pr2.*
- 42: gb_pr3.*
- 43: gb_sts.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
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1	354.4	99.6	356	10	S49899	S49899 alpha-globi
2	354.4	99.6	19226	11	HS6G4	Z84722 Human DNA s
3	354.4	99.6	356	40	S49899	S49899 alpha-globi
4	354.4	99.6	19226	41	HS6G4	Z84722 Human DNA s
5	102.2	28.7	277	13	S78508	S78508 alpha globi
6	102.2	28.7	330	13	MMU08220	U08220 Mus musculu
7	37.8	10.6	7218	6	I66494	I66494 Sequence 14
8	36.6	10.3	136019	18	HS327J16	AL008583 Human DNA
9	35.8	10.1	3905	11	HSB9HB1	U07663 Human HB9 h
10	35.8	10.1	3905	41	HSB9HB1	U07663 Human HB9 h
11	33.6	9.4	2844	6	I08667	I08667 Sequence 4
12	33.6	9.4	1858	10	HSPAI19	X13345 Human gene
13	33.6	9.4	1962	10	HSPAI19	X04744 Human mRNA
14	33.6	9.4	2876	10	HUMPA1A	M16006 Human plas
15	33.6	9.4	17509	10	HUMPA1A	J03764 Human, plas
16	33.6	9.4	2937	10	HUMPA1B	M14083 Human beta-
17	33.6	9.4	134641	18	AC004876	AC004876 *** SEQUE
18	33.6	9.4	1858	40	HSPAI19	X13345 Human gene
19	33.6	9.4	1962	40	HSPAI19	X04744 Human mRNA
20	33.6	9.4	2876	40	HUMPA1A	M16006 Human plas
21	33.6	9.4	17509	40	HUMPA1A	J03764 Human, plas
22	33.6	9.4	2937	40	HUMPA1B	M14083 Human beta-
23	33.4	9.4	174311	3	AC004758	AC004758 Drosophil
24	33.4	9.4	89818	11	AC002126	AC002126 Homo sapi
25	33.4	9.4	34877	11	CH19R27740	AD000812 Homo sapi
26	33.4	9.4	170891	18	AC002118	AC002118 *** SEQUE
27	33.4	9.4	89818	41	AC002126	AC002126 Homo sapi
28	33.4	9.4	34877	41	CH19R27740	AD000812 Homo sapi
29	33	9.3	1149	10	HSPKCG5	X62533 H.sapiens g
30	33	9.3	1149	40	HSPKCG5	X62533 H.sapiens g
31	32.8	9.2	325	43	HSC003ZA5	Z53931 H.sapiens (
32	32.6	9.2	1873	6	AR001351	AR001351 Sequence
33	32.6	9.2	1873	6	AR002247	AR002247 Sequence
34	32.6	9.2	1873	6	I15560	I15560 Sequence 24
35	32.6	9.2	1873	6	I56648	I56648 Sequence 18
36	32.6	9.2	1873	6	I58411	I58411 Sequence 5
37	32.6	9.2	1873	6	I58687	I58687 Sequence 18
38	32.6	9.2	1873	6	I60517	I60517 Sequence 18
39	32.6	9.2	1873	6	I68197	I68197 Sequence 18
40	32.6	9.2	1873	6	I79527	I79527 Sequence 18
41	32.6	9.2	1873	6	I83789	I83789 Sequence 24
42	32.6	9.2	1873	6	I96042	I96042 Sequence 18
43	32.6	9.2	2351	10	HSRNACPG8	X89430 H.sapiens m
44	32.6	9.2	112756	11	AF030876	AF030876 Homo sapi
45	32.6	9.2	2351	40	HSRNACPG8	X89430 H.sapiens m

ALIGNMENTS

RESULT	1	S49899	356 bp	DNA	PRI	10-JUL-1992
LOCUS	S49899	alpha-globin gene cluster: [5' region, major regulatory element]				
DEFINITION	S49899	[human, Genomic, 356 nt].				
ACCESSION	S49899	g233777				
NID	S49899	human.				
KEYWORDS	S49899	human.				
SOURCE	S49899	human.				
ORGANISM	S49899	Homo sapiens				
REFERENCE	S49899	Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 356)				
AUTHORS	S49899	Jarman, A.P., Wood, W.G., Sharpe, J.A., Gourdon, G., Ayyub, H. and Higgins, D.R.				
TITLE	S49899	Characterization of the major regulatory element upstream of the human alpha-globin gene cluster				
JOURNAL	S49899	Mol. Cell. Biol. 11 (9), 4679-4689 (1991)				
MEDLINE	S49899	91342671				
REMARK	S49899	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 49899] from the original journal article. This sequence comes from fig 5.				
COMMENT	S49899	Region: alpha-globin gene cluster.				

Db 10953 TCGACCTCTGGAACCTATCAGGACCAACAGTCAGCCAGGCAAGCACATCTGCCCAAGCC 11012

QY 61 aagggtgagggcagctgagctgtgggggtctgtgaaacacacttgaggagcagataactgg 120

Db 11013 AAGGTTGGAGGCATGAGCTGTGGGGTCTGTGAAACACACTTGGAGGACGAGATACTGG 11072

QY 121 gcaacacatgactcagctgcttctgaggagcacaagactcttgatcctcgtggtgggt 180

Db 11073 GCCAACCATGACTCAGTGTCTCTGGAGGCCAACAGACTGCTGAGTCATCCTGTGGGGGT 11132

QY 181 ggaagtggaaggaaggaaggggtgaatgactgtgattacaacctctgtgtgct 240

Db 11133 GGAGTGGGACAGGGAAGGGGTGAATGTTCTGATTACACCTCTGGTGTGCT 11192

QY 241 cccctctcttattctatgagaggaagccatgcccacaaagtgttcacagccaggtctcag 300

Db 11193 CCCCCTCTCTTATCTGAGAGGAAGGCCATGCCCAAAGTGTTCACAGCCAGGCTTCAG 11252

QY 301 gggcaagcctgaccagacagtaaatcgttcttcattctgagctgaagaaattc 356

Db 11253 GGGCAAGCCTGACCAGACAGTAATAGTCTTCTGCTGAGGCTGAAGAAATTC 11308

RESULT 3

S49899

LOCUS S49899 356 bp DNA PRI 10-JUL-1992

DEFINITION alpha-globin gene cluster: [5' region, major regulatory element]

ACCESSION S49899

NID g233777

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 356)

AUTHORS Jarman, A.P., Wood, W.G., Sharpe, J.A., Gourdon, G., Ayyub, H. and Higgs, D.R.

TITLE Characterization of the major regulatory element upstream of the human alpha-globin gene cluster

JOURNAL Mol. Cell. Biol. 11 (9), 4679-4689 (1991)

MEDLINE 91342671

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gbbseq 49899] from the original journal article. This sequence comes from fig 5.

COMMENT Region: alpha-globin gene cluster.

FEATURES

source

1..356

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 89 a 89 c 108 g 70 t

ORIGIN

Query Match 99.6%; Score 354.4; DB 40; Length 356;

Best Local Similarity 99.7%; Pred. No. 6.9e-103;

Matches 355; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcgacctctggaacctatcaggagcacacagtcagccaggcagcacatctgcccagcc 60

Db 1 TCGACCTCTGGAACCTATCAGGACCAACAGTCAGCCAGGCAAGCACATCTGCCAAGCC 60

QY 61 aagggtgagggcagctgagctgtgggggtctgtgaaacacacttgaggagcagataactgg 120

Db 61 AAGGTTGGAGGCATGAGCTGTGGGGTCTGTGAAACACACTTGGAGGACGAGATACTGG 120

QY 121 gcaacacatgactcagctgcttctgaggagcacaagactctgagctcctgtgggt 180

Db 121 GCCAACCATGACTCAGTGTCTCTGGAGGCCAACAGACTGCTGAGTCATCCTGTGGGGGT 180

QY 181 ggaagtggaaggaaggaaggggtgaatgactgtgattacaacctctgtgtgct 240

Db 181 GGAGTGGGACAGGAAGGGGTGAATGTTCTGCTGATTACAACTCTGTTGTGCTGCT 240

QY 241 cccctctctgtttatctgagagggagccatgcccaagtgttcacagccaggtctcag 300

Db 241 CCCCCTCTCTGTTATCTGAGAGGGAAGCCATGCCCAAAGTGTTCACAGCCAGGCTTCAG 300

QY 301 gggcaagcctgaccagacagtaaatcgttcttcattctgagactgaagaaattc 356

Db 301 GGGCAAGCCTGACCAGACAGTAATAGTCTTCTGCTGAGGCTGAAGAAATTC 356

RESULT 4

HS6G4

LOCUS HS6G4 19226 bp DNA PRI 19-MAR-1997

DEFINITION Human DNA sequence from cosmid G64 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3.

ACCESSION 284722

NID g1817579

KEYWORDS 16p13.3.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 19226)

AUTHORS Flint, J. and Higgs, D.R.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-1997) Sanger Centre, 970124/Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk

COMMENT IMPORTANT: this sequence is not the entire insert of clone G64. This clone was sequenced at the Institute of Molecular Medicine. The true left end of clone G64 is at 1 in this sequence. The true right end of clone RA36 is at 456. The true left end of clone PX94 is at 19090. G64 is from a 280kb clone contig extending from the telomere of 16p.

Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.

G64 came from the Los Alamos, flow sorted human Chromosome 16 library.

FEATURES

source

1..19226

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="16"

/map="16p13.3"

/clone="G64"

601..894

/note="AluJb repeat: matches 301..5 of consensus"

repeat_region

1156..1290

/note="AluX repeat: matches 1..136 of consensus; incomplete repeat"

repeat_region

1291..1601

/note="AluS repeat: matches 1..300 of consensus"

1602..1758

/note="AluS repeat: matches 132..288 of consensus; incomplete repeat"

repeat_region

3487..3784

/note="AluS repeat: matches 1..299 of consensus"

3809..4104

/note="AluJo repeat: matches 1..302 of consensus"

4823..5030

/note="AluS repeat: matches 2..208 of consensus; incomplete repeat"

repeat_region

5053..5092

/note="20 copies of 2 mer 85 % conserved"

5122..5280

/note="FAM repeat: matches 164..5 of consensus"

5759..5903

/note="LMC2 repeat: matches 169..321 of consensus"

6130..6427

/note="AluS repeat: matches 297..1 of consensus"

6428..6724

/note="AluJo repeat: matches 299..1 of consensus"

7144..7265

[illegible]


```

      exon      /note="PAI-1, intron D"
      9747. .9945
      /number=5
      intron     9946. .11537
      /note="PAI-1, intron E"
      exon      11538. .11638
      /number=6
      intron     11639. .11757
      /note="PAI-1, intron F"
      exon      11758. .11844
      /number=7
      intron     11845. .13052
      /note="PAI-1, intron G"
      exon      13053. .13136
      /number=8
      intron     13137. .13456
      /note="PAI-1, intron H"
      exon      13457. .>13494
      /note="plasma1nogen activator-1"
      /number=9

BASE COUNT      4974 a 4406 c 4386 g 3743 t
ORIGIN          131 bp upstream of SacI site; chromosome 7q21.3-q22.

Query Match      9.4%; Score 33.6; DB 10; Length 17509;
Best Local Similarity 48.0%; Pred. No. 2.5;
Matches 96; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY  95 aaacacttgaggagcagataactggccaaccatgactcagtgcttcttgaggccaaca 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  14196 AAAAATAAAGGAGCAGAAATCTGCTCAATGAGTAACAAGTCACCTACACTCCAAA 14137

QY  155 ggactcttgagtcactcctgtggggtgaggtgggacaagggaagggtgaatggtact 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  14136 TAACCCATGCACACTGTTCTCGGGGAGGAGATGCCAGGCCAGGAGATTGGGCCACAT 14077

QY  215 gctgattacaacctgtgtgctgcctccctctctgtttatctgagagggaaggccatgc 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  14076 GATGGGGACATTCACCTCTGCCACCTGCAGCACCCCTGTACTGGGGAGGGGTGCCAGTG 14017

QY  275 ccaaagtgttcacagccagg 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  14016 CCACAGTGGACTCTGAGATG 13997
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Search completed: June 24, 1999, 01:30:43
Job time: 3031 sec

